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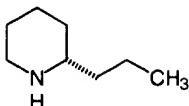
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igase

Conium maculatum. The natural enantiomer has *S* conformation.



igase γ -Glu-X carboxypeptidase, EC 3.4.19.9 (formerly 3.4.22.12); γ -glutamyl hydrolase; an enzyme that hydrolyses γ -glutamyl bonds in *N*-pteroyl- γ -oligoglutamate, pteroyl-glutamate being a prominent product.

igate 1 to effect or undergo **conjugation**. 2 describing either of a pair of interconvertible substances, e.g. a **conjugate acid-base pair**. 3 the product formed as a result of conjugation.

igate acid-base pair the relationship between two chemicals, BH^+ and *B*, that are related by the reaction: $BH^+ + H^+$. Then BH^+ is the **conjugate acid** of the base *B*, *B* is **conjugate base** of the acid BH^+ , and BH^+ and *B* are a **conjugate acid-base pair**.

igate base see **conjugate acid-base pair**.

igated 1 describing a compound that is formed by the joining of two compounds. 2 displaying or having undergone **igation**.

igated double bond any of two or more double bonds in a molecule where each double bond is separated from the next by one single bond. Compare **conjugation** (def. 2).

igated protein any protein that contains a nonprotein component, often in stoichiometric proportion. The nonprotein component may be a metal ion, a lipid, a carbohydrate, or nucleic acid, and may be either loosely or tightly bound to polypeptide chain(s).

igation 1 the act of joining together; the state of being joined together. 2 an alternating sequence of multiple and single chemical bonds containing at least two multiple bonds. Delocalization of pi-electrons and resultant additional stability. 3 the covalent or noncovalent joining together of one (larger) molecule, e.g. a protein or bile acid, with a second (smaller) molecule. 4 a process of sexual reproduction occurring in various types of unicellular organisms. In bacteria, e.g. *Escherichia coli*, it involves the transfer of DNA from a donor cell to a recipient cell via a sex pilus; in protozoa, *Paramecium aurelia*, a true exchange of DNA occurs between the participating cells, which belong to different mating types.

igation labelling a procedure for introducing a label into a molecule of interest by covalently coupling it, in a specific chemical reaction, to a small molecule containing the label (see **conjugation** (def. 3)). It is particularly useful for labelling with radioiodine any protein or peptide that is sensitive to oxidative procedures or to noxious components of medical radioiodine, that lacks tyrosine residues reactive with iodine, or that requires to be labelled at a residue other than tyrosine. See also **Bolton and Hunter reagent**.

igative plasmid any plasmid that can bring about the transfer of DNA by **conjugation** (def. 3).

igon any genetic element that is required for bacterial **igation** (def. 4), e.g. **fertility factor**.

igactive tissue any supporting tissue that lies between other tissues and consists of cells embedded in a relatively large amount of extracellular matrix.

igactive tissue growth factor abbr.: CTGF; a growth factor of testis, spleen, kidney, lung, heart, and brain, that is similar to **CEF10**, one of a family of growth regulators that belong to a group of immediate-early genes expressed after induction by growth factors or certain oncogenes. The family includes **Cyr61**, **BIG-M1**, and **BIG-M2**. Example (precursor) in mouse: database code **CTGF_MOUSE**, 348 amino acids (5 kDa).

connectivity (in chemistry) the information in any molecular formula or model regarding the order in which the constituent atoms of the molecule are linked, irrespective of the nature of the linkages.

connexin the main protein component of a **connexon**. Each connexin contains four putative membrane-spanning α -helices, and six connexins make up each connexon. A number of different subtypes of connexin exist within each species, contributing different functional behaviour to different connexons. Example from human: database code **CX26_HUMAN**, 208 amino acids (24.27 kDa); four motifs.

connexon the structural subunit of a **gap junction**, the structure that forms a bridge between adjacent cells in certain tissues of vertebrates. Seen by electron microscopy or low-angle X-ray diffraction, an individual gap junction consists of a number (10–10⁴) of connexons, often in hexagonal array, embedded in and protruding from either side of each of the opposed cell membranes in register and linked to one another. Each connexon is a cylindrical proteinaceous structure, about 6–8.5 nm in diameter and 7.5 nm long; it consists of six rod-shaped, essentially rigid subunits (**connexins**) of about 25 kDa arranged in an annulus. The diameter of the central opening can apparently be varied by radial displacement of the subunits at their cytoplasmic extremities. Each connexin spans one cell membrane, two with connecting ends being required to form a channel across both membranes. Such channels provide a regulable hydrophilic pathway permitting the passage of small molecules (up to about 800 Da) between adjacent cells; the specificity of each channel is determined by the type of connexin it utilizes.

conotoxin abbr.: ω -CT; any of several peptides of the family of ω -conotoxins isolated from the venoms of two marine snails, *Conus geographicus* and *C. magus*. All ω -conotoxins have a conserved pattern of cysteine residues linked by four disulfide bridges. They are neurotoxins that inhibit voltage-gated Ca^{2+} channels and neurotransmitter release. ω -Conotoxin GVIA has the structure:

[tricyclic (1→16, 8→19, 15→26)(H-Cys¹-Lys-Ser-Hyp-Gly-Ser-Ser-Cys⁸-Ser-Hyp-Thr-Ser-Tyr-Asn-Cys¹⁵-Cys¹⁶-Arg-Ser-Cys¹⁹-Asn-Hyp-Tyr-Thr-Lys-Arg-Cys²⁶-Tyr-NH₂)].

consensus sequence an idealized sequence of nucleotides, or their constituent bases, or amino acids, base, or amino acid that represents the nucleotide most likely to occur at each position in the sequence. Consensus sequences are used to identify RNA splicing sites, other sites, plasmids, and families of proteins.

conservation the retention of structure by a macromolecule, or by a specified segment of one, with variation of circumstance (environmental, genetic, etc.). When used of primary structure, it can be synonymous with **sequence homology**. The degree of retention of structure is usually specified. See also **conserved**.

conservation of energy (law of the) see **thermodynamics**.

conservative base change or **conservative base substitution** any mutational change, including substitution of a base, in a particular base triplet in a DNA molecule such that either the amino acid encoded by that base triplet is not altered, or there is no major change in the properties of the R group of the amino acids involved, e.g. Glu for Asp. See **genetic code**, **wobble hypothesis**.

conservative replacement or **conservative substitution** any replacement or substitution in a polypeptide chain of a particular amino acid residue by another one with similar properties, e.g. Arg for Lys, Phe for Tyr, Glu for Asp.

conserved describing a tendency to invariance in corresponding residues or sequences of residues of encoded macromolecules (e.g. proteins) obtained from specimens of genetically different sources. Macromolecules showing a high degree of